

The motor domain is amino acids 96–348 or base pair 143–1174.

Fig. 1A

601 GGTGTATAATGAACAGATCCATGACCTCCTGGAGCCCAAGGGGCCCCTTGCCATCCGCGA 660
 -----+-----+-----+-----+-----+-----+-----+
 uValTyrAsnGluGlnIleHisAspLeuLeuGluProLysGlyProLeuAlaIleArgG1
 5
 661 GGACCCCGACAAGGGGGTGGTGGTGAAGGACTTTCTTTCCACCAGCCAGCCTCAGCCGA 720
 -----+-----+-----+-----+-----+-----+-----+
 uAspProAspLysGlyValValValGlnGlyLeuSerPheHisGlnProAlaSerAlaG1
 10
 721 GCAGCTGCTGGAGATACTGACCAGGGGGAACCGTAACCGCACGCAGCACCCCACTGATGC 780
 -----+-----+-----+-----+-----+-----+-----+
 uGlnLeuLeuGluIleLeuThrArgGlyAsnArgAsnArgThrGlnHisProThrAspAl
 15
 781 CAACGCGACTTCCTCCCGCTCCCATGCCATCTTCCAGATCTTTGTGAAGCAGCAGGACCG 840
 -----+-----+-----+-----+-----+-----+-----+
 aAsnAlaThrSerSerArgSerHisAlaIlePheGlnIlePheValLysGlnGlnAspAr
 20
 841 GGTTCAGGACTGACCCAGGCTGTCCAGGTGGCCAAGATGAGCCTGATTGACCTGGCTGG 900
 -----+-----+-----+-----+-----+-----+-----+
 gValProGlyLeuThrGlnAlaValGlnValAlaLysMetSerLeuIleAspLeuAlaG1
 25
 901 CTCAGAGCGGGCATCCAGCACCCATGCGAAGGGGAGCGGCTGCGGGAGGGGGCCAACAT 960
 -----+-----+-----+-----+-----+-----+-----+
 ySerGluArgAlaSerSerThrHisAlaLysGlyGluArgLeuArgGluGlyAlaAsnIl
 30
 961 CAACCGCTCTCTGCTGGCGCTCATCAACGTCCTCAATGCCTTGGCCGATGCAAAGGGCCG 1020
 -----+-----+-----+-----+-----+-----+-----+
 eAsnArgSerLeuLeuAlaLeuIleAsnValLeuAsnAlaLeuAlaAspAlaLysGlyAr
 35
 1021 CAAGACCCATGTGCCCTACCGGGACAGCAAAGTACCCGCCTGCTCAAAGACTCCCTCGG 1080
 -----+-----+-----+-----+-----+-----+-----+
 gLysThrHisValProTyrArgAspSerLysLeuThrArgLeuLeuLysAspSerLeuG1
 40
 1081 GGGCAACTGCCGACAGTGATGATCGCTGCCATCAGCCCCTCCAGCCTGACCTACGAGGA 1140
 -----+-----+-----+-----+-----+-----+-----+
 yGlyAsnCysArgThrValMetIleAlaAlaIleSerProSerSerLeuThrTyrGluAs
 45
 1141 CACGTACAACACCCTCAAATATGCCGACCGGGGCCAAGGAGATCAGGCTCTCGCTGAAGAG 1200
 -----+-----+-----+-----+-----+-----+-----+
 pThrTyrAsnThrLeuLysTyrAlaAspArgAlaLysGluIleArgLeuSerLeuLysSe
 50
 1201 CAATGTGACCAGCCTGGACTGTACATCAGCCAGTATGCTACCATCTGCCAACAGCTCCA 1260
 -----+-----+-----+-----+-----+-----+-----+
 rAsnValThrSerLeuAspCysHisIleSerGlnTyrAlaThrIleCysGlnGlnLeuG1
 55

Fig. 1B

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1261 GGCTGAGGTAGCCGCTCTGAGGAAGAAGCTCCAAGTGTATGAGGGGGGAGGCCAGCCCCC 1320
-----+-----+-----+-----+-----+-----+
nAlaGluValAlaAlaLeuArgLysLysLeuGlnValTyrGluGlyGlyGlyGlnProPr

1321 ACCACAGGACCTCCCAGGATCTCCCAAGTCGGGACCACCACCAGAACACCTTCCCAGCTC 1380
-----+-----+-----+-----+-----+-----+
oProGlnAspLeuProGlySerProLysSerGlyProProProGluHisLeuProSerSe

1381 CCCCTTGCCACCCACCCCTCCCAGCCAGCCCTGCACCCACAGACTCCCTGCAGGGCCTAG 1440
-----+-----+-----+-----+-----+-----+
rProLeuProProHisProProSerGlnProCysThrProGluLeuProAlaGlyProAr

1441 AGCCCTTCAAGAGGAGAGTCTGGGGATGGAGGCCAGGTGGAGAGGGCCATGGAAGGGAA 1500
-----+-----+-----+-----+-----+-----+
gAlaLeuGlnGluGluSerLeuGlyMetGluAlaGlnValGluArgAlaMetGluGlyAs

1501 CTCTTCAGACCAGGAGCAGTCCCCAGAGGATGAGGATGAAGGCCAGCTGAGGAGGTTC 1560
-----+-----+-----+-----+-----+-----+
nSerSerAspGlnGluGlnSerProGluAspGluAspGluGlyProAlaGluGluValPr

1561 AACCAGATGCCAGAGCAGAACCCACACATGCACTGCCAGAGTCCCCTCGCTGACCCCT 1620
-----+-----+-----+-----+-----+-----+
oThrGlnMetProGluGlnAsnProThrHisAlaLeuProGluSerProArgLeuThrLe

1621 GCAGCCCAAGCCAGTCGTGGGCCACTTCTCAGCACGGGAACTGGATGGGGACCGTTCTAA 1680
-----+-----+-----+-----+-----+-----+
uGlnProLysProValValGlyHisPheSerAlaArgGluLeuAspGlyAspArgSerLy

1681 GCAGTTGGCCCTAAAGGTGCTGTGCGTTGCCAGCGGCAGTACTCCCTGCTCCAAGCAGC 1740
-----+-----+-----+-----+-----+-----+
sGlnLeuAlaLeuLysValLeuCysValAlaGlnArgGlnTyrSerLeuLeuGlnAlaAl

1741 CAACCTCCTGACGCCCCGACATGATCACAGAGTTTGAGACCCTACAGCAGCTGGTGCAAGA 1800
-----+-----+-----+-----+-----+-----+
aAsnLeuLeuThrProAspMetIleThrGluPheGluThrLeuGlnGlnLeuValGlnGl

1801 GGAAAAAATTGAGCCTGGGGCAGAGGCCTTGAGGACTTCAGGCCTGGCCAGGGGGGCACC 1860
-----+-----+-----+-----+-----+-----+
uGluLysIleGluProGlyAlaGluAlaLeuArgThrSerGlyLeuAlaArgGlyAlaPr

1861 TCTGGCTCAGGAGCTGTGTTTCAGAGTCAATCCCTGTGCCGTCTCCTCTCTGCCAGAGCC 1920
-----+-----+-----+-----+-----+-----+
oLeuAlaGlnGluLeuCysSerGluSerIleProValProSerProLeuCysProGluPr

Fig. 1C

1921 TCCAGGATACACTGGCCCTGTGACCCGACTATGGCGAGGCGACTGAGTGGCCCCCTGCA 1980
-----+-----+-----+-----+-----+-----+
oProGlyTyrThrGlyProValThrArgThrMetAlaArgArgLeuSerGlyProLeuHi

1981 CACCCTGGGAATCCCGCCTGGACCCAACTGCACCCAGCCAGGGGTCCCGATGGCCCAT 2040
-----+-----+-----+-----+-----+-----+
sThrLeuGlyIleProProGlyProAsnCysThrProAlaGlnGlySerArgTrpProMe

2041 GGAGAAGAAGAGGAGGAGACCAAGCGCCTTGGAGGCAGACAGTCCCATGGCCTCAAAGCG 2100
-----+-----+-----+-----+-----+-----+
tGluLysLysArgArgArgProSerAlaLeuGluAlaAspSerProMetAlaSerLysAr

2101 GGGCACCAAGCGCCAGCGCCAGTCCTTCTGCCCCTGCCTAAGGAGAGGGTCTCTGCCTGA 2160
-----+-----+-----+-----+-----+-----+
gGlyThrLysArgGlnArgGlnSerPheLeuProCysLeuArgArgGlySerLeuProAs

2161 CACCCAACCTTCACAGGGGCCAGCACCCCCAAAGGAGAAAGGGCCTCCTCCCCCTGCCA 2220
-----+-----+-----+-----+-----+-----+
pThrGlnProSerGlnGlyProSerThrProLysGlyGluArgAlaSerSerProCysHi

2221 TTCCCCCTCGCGTTTGCCCAGCCACAGTCATCAAAAGCCGGGTGCCCTGGGCCCCTTCCGC 2280
-----+-----+-----+-----+-----+-----+
sSerProArgValCysProAlaThrValIleLysSerArgValProLeuGlyProSerAl

2281 CATGCAGAACTGCTCCACCCCGCTGGCTCTGCCCACTCGAGACCTCAATGCCACCTTTGA 2340
-----+-----+-----+-----+-----+-----+
aMetGlnAsnCysSerThrProLeuAlaLeuProThrArgAspLeuAsnAlaThrPheAs

2341 TCTCTCTGAGGAGCCTCCCTCAAAGCCAGTTTCCATGAATGCATTGGCTGGGACAAAAA 2400
-----+-----+-----+-----+-----+-----+
pLeuSerGluGluProProSerLysProSerPheHisGluCysIleGlyTrpAspLysIl

2401 ACCCCAGGAGCTGAGCAGGCTGGACCAGCCCTTCATCCCCAGGGCACCTGTGCCCTGT 2460
-----+-----+-----+-----+-----+-----+
eProGlnGluLeuSerArgLeuAspGlnProPheIleProArgAlaProValProLeuPh

2461 CACCATGAAGGGCCCCAAGCCAACATCTTCCCTCCCTGGGACCTCTGCCTGCAAGAAGAA 2520
-----+-----+-----+-----+-----+-----+
eThrMetLysGlyProLysProThrSerSerLeuProGlyThrSerAlaCysLysLysLy

2521 GCGCGTTGCGAGTTCCTCAGTCTCCCATGGCCGCGAGCCGCATCGCCCGCCTCCCGAGCAG 2580
-----+-----+-----+-----+-----+-----+
sArgValAlaSerSerSerValSerHisGlyArgSerArgIleAlaArgLeuProSerSe

Fig. 1D

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2581 CACTTTGAAGAGGCCAGCTGGGCCCCCTTGTA TCTCCAGAGCTGCCCTTGAGTCCCCTGTG
-----+-----+-----+-----+-----+ 2640
rThrLeuLysArgProAlaGlyProLeuValLeuProGluLeuProLeuSerProLeuCy

2641 CCCTAGCAACCGGAGGAATGGAAAGGACCTCATCAGGGTGGGGAGAGCGCTCTCAGCAGG
-----+-----+-----+-----+-----+ 2700
sProSerAsnArgArgAsnGlyLysAspLeuIleArgValGlyArgAlaLeuSerAlaGl

2701 GAACGGCGTCACCAAGGTGTCCTGACCGCCAGAATGTCCTGACCACCAAGGTGTCCTAAC
-----+-----+-----+-----+-----+ 2760
yAsnGlyValThrLysValSer

2761 CTACCGGCCCCCTCTGCTGGATACCCCTCTTGACCTGTAGCCACCTGCACCAGGAGCTGG
-----+-----+-----+-----+-----+ 2820

2821 ACCTGCCTTCCTTACCTGGGAGCAATTAGTGCCAACACACCTTTGCTGTATTAACATCCC
-----+-----+-----+-----+-----+ 2880

2881 TCCCCAGACATCCATCCTGCTACTCACCCCTCTGTTAATCTCCTGTTAACTCAGCTTCTT
-----+-----+-----+-----+-----+ 2940

2941 GGCATGTACATATTCATTTGTGAGTGTTAATGTGCTGCTGTTTTTTGTTTTTGGTGGTT
-----+-----+-----+-----+-----+ 3000

3001 TTTGTTTTTTGTTTTTTTGTGTTTGGAGATGGAGTCTTACTCTGTCGCCCAGGCTGGAGTG
-----+-----+-----+-----+-----+ 3060

3061 CAGTGGTACGATCTTGCTCACTGCAACCTCCGCCTCCTGGGTTCAAGTAATTCTCCTGC
-----+-----+-----+-----+-----+ 3120

3121 CTCAGCTTTCCAAGTAGCTGGGATTACAGGCACCCATCACCACACCCAGCTAATTTTCGT
-----+-----+-----+-----+-----+ 3180

3181 CTTTTTAATAGAGAGGGGGTTTTTCCATGTTGGCCAGGCTGGTCTTGAACCTCCTGACCTC
-----+-----+-----+-----+-----+ 3240

3241 AGGTGATCCGCCTGCCTCAGCTTCCCAAAGTGCTGAGATTACAGGCATGAGCTACCACGC
-----+-----+-----+-----+-----+ 3300

3301 CTGGCCCGTGTGCTGTTTTTAAAGGTGCTGCCATGTTCCCCCATCTTTTTTTTTTTTGAG
-----+-----+-----+-----+-----+ 3360

Fig. 1E

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3361 ATGGAGTCTCGCTCTGTGCGCCAGGCTGGAGTGCAGTGGTGGCGATCTTGGCTCACTGCA
-----+-----+-----+-----+-----+-----+ 3420

3421 AGCTCCGCCTCCCAGGTTACACCATTTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTA
-----+-----+-----+-----+-----+-----+ 3480

3481 CAGGCGCCACACCACGCGCCGGCTAATTTTTGTATTTTAGTAGAGATGGGGTTTCAC
-----+-----+-----+-----+-----+-----+ 3540

3541 CGTGTTAGCCAGGCTGGTCTCGATCTGACCTCATGATCCACCCGCTCGGCCTCCCAAAG
-----+-----+-----+-----+-----+-----+ 3600

3601 TGCTGGGATTACAGGCGTGAGCCACTGCGCCCGGCCTCCCCTCTCATTTATGATGCCCTC
-----+-----+-----+-----+-----+-----+ 3660

3661 TGTGCAGGCAGACGGCTCTTGGGCTCTTTCCCCACCTGTCTCTAACACAGGCCCCACGG
-----+-----+-----+-----+-----+-----+ 3720

3721 TGATGGCCACAGGCAGTAGAGGAGGAATGAGGATGGGTGGGGAGCGGGGAGTCGCGGCT
-----+-----+-----+-----+-----+-----+ 3780

3781 TGGCTCTTCCTGGTTTCTGAGAGGGACATCTTCATCCCTACTCCCCTTGGTCCCCAACCA
-----+-----+-----+-----+-----+-----+ 3840

3841 CAGTCCTGGTGAAGATGTGGATGATAATGGTGCCTTGATTCCAAATGAAGACAGCTTTA
-----+-----+-----+-----+-----+-----+ 3900

3901 TTGCTTAACTCTATTGTACATAGGATACACGTTCAAGTGTAATAAAGTGTAAGGGGAA
-----+-----+-----+-----+-----+-----+ 3960

3961 TTCAGGCTTAATGCTGCACCTAGATATAAATGCTAATGATACTTGGGTTTATAGCCTTCT
-----+-----+-----+-----+-----+-----+ 4020

4021 GATCCTTTATTTCTGCATATATATATAGATATATACATATATTTTGGTATAACAATAAA
-----+-----+-----+-----+-----+-----+ 4080

4081 CCGTCTCCATCCTTGGGAAAAAAAAAAAA 4108

Fig. 1F.

DNA sequence of HsKIP3A, motor only

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1   GACAGCACGC TGCAAGTAGT GGTACGGGTG CGGCCCCCCA CCCCTCGGGA GCTGGACAGT
61  CAGCGGCGGC CAGTGGTTCA GGTGGTGGAC GAGCGGGTGC TGGTGTTTAA CCCTGAGGAG
5  121 CCCGATGGAG GGTTCCTTGG CCTGAAATGG GGTGGCACCC ATGATGGCCC CAAGAAGAAG
181 GGCAAAGACC TGACGTTTGT CTTTGACCGG GTCTTTGGCG AGGCGGCCAC CCAACAGGAC
241 GTGTTCCAGC ACACCACGCA CAGCGTCCTG GACAGCTTCC TCCAGGGCTA CAACTGCTCA
301 GTGTTTGCCT ACGGGGCCAC CGGGGCTGGG AAGACACACA CCATGCTGGG AAGGGAGGGG
10 361 GACCCCGGCA TCATGTACCT GACCACCGTG GAACTGTACA GGCGCCTGGA GGCCCGCCAG
421 CAGGAGAAGC ACTTCGAGGT GCTCATCAGC TACCAGGAGG TGTATAATGA ACAGATCCAT
481 GACCTCCTGG AGCCCAAGGG GCCCCTTGCC ATCCGCGAGG ACCCCGACAA GGGGGTGGTG
541 GTGCAAGGAC TTTCTTTCCA CCAGCCAGCC TCAGCCGAGC AGCTGCTGGA GATACTGACC
601 AGGGGGAACC GTAACCGCAC GCAGCACCCC ACTGATGCCA ACGCGACTTC CTCCCGCTCC
15 661 CATGCCATCT TCCAGATCTT TGTGAAGCAG CAGGACCGGG TTCCAGGACT GACCCAGGCT
721 GTCCAGGTGG CCAAGATGAG CCTGATTGAC CTGGCTGGCT CAGAGCGGGC ATCCAGCACC
781 CATGCGAAGG GGGAGCGGCT GCGGGAGGGG GCCAACATCA ACCGCTCTCT GCTGGCGCTC
841 ATCAACGTCC TCAATGCCTT GGCCGATGCA AAGGGCCGCA AGACCCATGT GCCCTACCGG
901 GACAGCAAAC TGACCCGCCT GCTCAAAGAC TCCCTCGGGG GCAACTGCCG CACAGTGATG
20 961 ATCGCTGCCA TCAGCCCCTC CAGCCTGACC TACGAGGACA CGTACAACAC CCTC

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Fig. 2

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Protein sequence of HsKIP3A, motor only

5 1 DSTLQVVVRV RPPTPRELDS QRRPVVQVVD ERVLVFNPEE PDGGFPGLKW GGTHDGPKKK
 61 GKDLTFVFDR VFGEAATQQD VFQHTTHSVL DSFLQGYNCS VFAYGATGAG KTHTMLGREG
 121 DPGIMYLTIV ELYRRLEARQ QEKHFVVLIS YQEVYNEQIH DLLEPKGPLA IREDPDKGVV
 181 VQGLSFHQPA SAEQLLEILT RGNRNRTQHP TDANATSSRS HAIFQIFVKQ QDRVPGLTQA
 241 VQVAKMSLID LAGSERASST HAKGERLREG ANINRSLAL INVLNALADA KGRKTHVPYR
 301 DSKLTRLLKD SLGGNCRTVM IAAISPSILT YEDTYNTL

10 Fig. 3

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Figure 4:

MAVEDSTLQVVVRVRPPTPRELDSQRRPVVQVVDERVLVFNPEEPDGGFPGLKWGGT
 HDGPKKKGKDLTFVFDRLFGEAATQQDVFOHTTHSVLDSFLQGYNCVFAVGATGAG
 KTHTMLGREGDPGIMYLTVELYRRLEARQQEKHFEVLISYQEVYNEQIHDLLLEPKG
 5 PLAIREDPDKGVVVQGLSFHQPASAEQLLEILTRGNRNRTQHPTDANATSSRSHAIF
 QIFVKQQDRVPGLTQAVQVAKMSLIDLAGSERASSTHAKGERLREGANINRSLALI
 NVLNALADAKGRKTHVPYRDSKLTRLKDSLGGNCRTVMIAAISPSSTLYEDTYNTL
 KYADRAKEIRLKGNSKLEGKPIPNPLLGLDSTRTGHHHHHH

- 10 Grayed sequence is derived from the vector (pCRT7/CT, Invitrogen) and contains a V5 epitope and polyhistidine tag.

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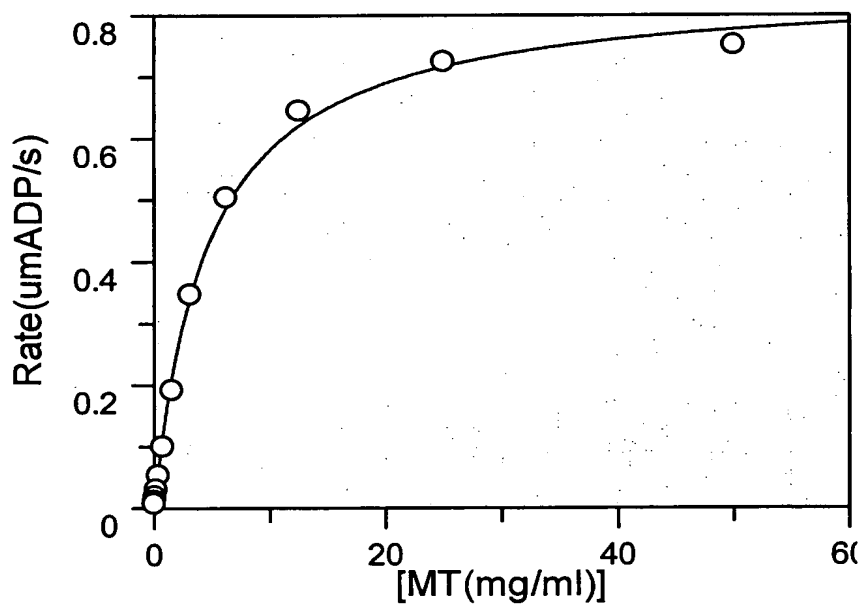
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Figure 5: Nucleotide sequence of the Kip3a fragment used in the ATPase assay

ATGGCAGTGGAGGACAGCACGCTGCAAGTAGTGGTACGGGTGCGGCCCCCACCCT
CGGGAGCTGGACAGTCAGCGGCGGCCAGTGGTTCAGGTGGTGGACGAGCGGGTGCTG
5 GTGTTTAACCCTGAGGAGCCCGATGGAGGGTTCCCTGGCCTGAAATGGGGTGGCACC
CATGATGGCCCCAAGAAGAAGGGCAAAGACCTGACGTTTGTCTTTGACCGGTCTTT
GGCGAGGCGGCCACCCAACAGGACGTGTTCCAGCACACCACGCACAGCGTCCTGGAC
AGCTTCCTCCAGGGCTACAACCTGCTCAGTGTTTGCCTACGGGGCCACCGGGGCTGGG
AAGACACACACCATGCTGGGAAGGGAGGGGGACCCCGGCATCATGTACCTGACCACC
10 GTGGAACCTGTACAGGCGCCTGGAGGCCCGCCAGCAGGAGAAGCACTTCGAGGTGCTC
ATCAGCTACCAGGAGGTGTATAATGAACAGATCCATGACCTCCTGGAGCCCAAGGGG
CCCCTTGCCATCCGCGAGGACCCCGACAAGGGGGTGGTGGTGC AAGGACTTTCTTTC
CACCAGCCAGCCTCAGCCGAGCAGCTGCTGGAGATACTGACCAGGGGGAACCGTAAC
CGCACGCAGCACCCCACTGATGCCAACGCGACTTCCTCCCGCTCCCATGCCATCTTC
15 CAGATCTTTGTGAAGCAGCAGGACCGGGTTCCAGGACTGACCAGGCTGTCCAGGTG
GCCAAGATGAGCCTGATTGACCTGGCTGGCTCAGAGCGGGCATCCAGCACCCATGCG
AAGGGGGAGCGGCTGCGGGAGGGGGCCAACATCAACCGCTCTCTGCTGGCGCTCATC
AACGTCCTCAATGCCTTGCGCGATGCAAAGGGCCGCAAGACCCATGTGCCCTACCGG
GACAGCAAACCTGACCCGCCTGCTCAAAGACTCCCTCGGGGGCAACTGCCGCACAGTG
20 ATGATCGCTGCCATCAGCCCCTCCAGCCTGACCTACGAGGACACGTACAACACCCTC
AAATATGCCGACCGGGCCAAGGAGATCAGGCTCAAGGGCAATTCCAAGCTTGAAGGT
AAGCCTATCCCTAACCCCTCTCCTCGGTCTCGATTCTACGCGTACCGGTCATCATCAC
CATCACCATTGA

- 25 Grayed sequence is derived from the vector (pCRT7/CT, Invitrogen) and contains a V5 epitope and polyhistidine tag.

Fig. 6



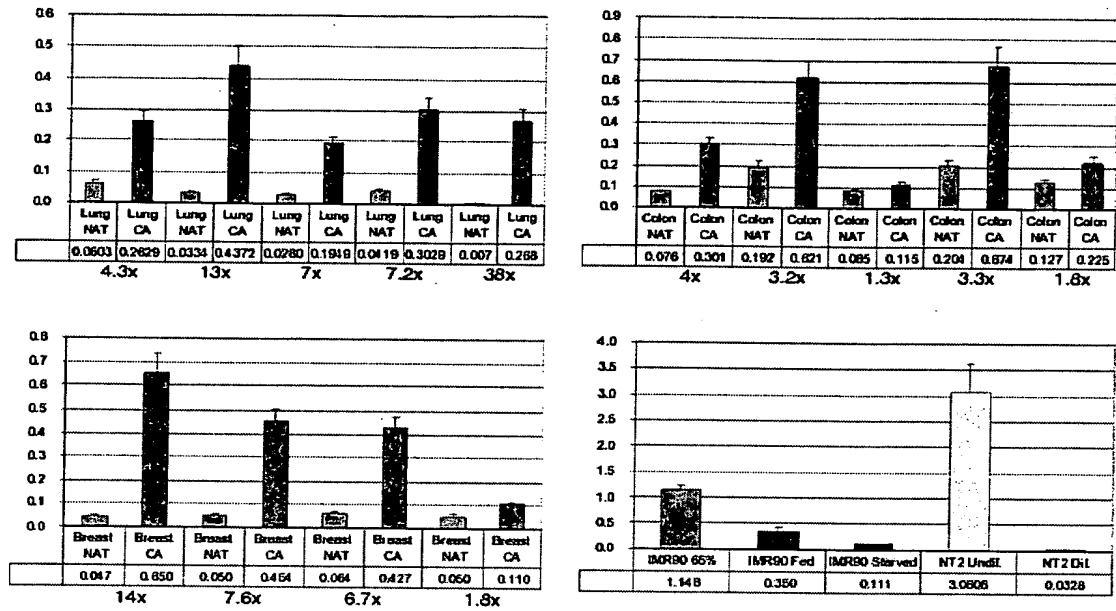
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5 Fig. 7

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